



## SEQUENCE LISTING

<110> MORGAN, BRYAN P.  
RUSHMERE, NEIL K.  
HINCHLIFFE, STEWART J.  
VAN DEN BERG, CARMEN W.

<120> MODIFIED BIOLOGICAL MATERIAL

<130> WN/KH/JJ/WCM

<140> 10/759,181  
<141>

<150> PCT/GB99/01085  
<151> 1999-04-08

<150> GB 9807520.3  
<151> 1998-04-09

<160> 24

<170> PatentIn Ver. 2.1

<210> 1  
<211> 123  
<212> PRT  
<213> Porcus sp.

<400> 1

Met Gly Ser Lys Gly Gly Phe Ile Leu Leu Trp Leu Leu Ser Ile Leu  
1 5 10 15

Ala Val Leu Cys His Leu Gly His Ser Leu Gln Cys Tyr Asn Cys Ile  
20 25 30

Asn Pro Ala Gly Ser Cys Thr Thr Ala Met Asn Cys Ser His Asn Gln  
35 40 45

Asp Ala Cys Ile Phe Val Glu Ala Val Pro Pro Lys Thr Tyr Tyr Gln  
50 55 60

Cys Trp Arg Phe Asp Glu Cys Asn Phe Asp Phe Ile Ser Arg Asn Leu  
65 70 75 80

Ala Glu Lys Lys Leu Lys Tyr Asn Cys Cys Arg Lys Asp Leu Cys Asn  
85 90 95

Lys Ser Asp Ala Thr Ile Ser Ser Gly Lys Thr Ala Leu Leu Val Ile  
100 105 110

Leu Leu Leu Val Ala Thr Trp His Phe Cys Leu  
115 120

<210> 2  
<211> 773

<212> DNA  
<213> Porcus sp.

<220>  
<221> CDS  
<222> (90)..(458)

<400> 2

```
gaaaagacgc gcaggccggg ccgctctccc gacggggagt agcgctgcag ccggacgcag 60
ggtgcagtta gaatccatag acggtcacg atg gga agc aaa gga ggg ttc att 113
                               Met Gly Ser Lys Gly Gly Phe Ile
                               1           5

ttg ctc tgg ctc ctg tcc atc ctg gct gtt ctc tgc cac tta ggt cac 161
Leu Leu Trp Leu Leu Ser Ile Leu Ala Val Leu Cys His Leu Gly His
   10           15           20

agc ctg cag tgc tat aac tgt atc aac cca gct ggt agc tgc act acg 209
Ser Leu Gln Cys Tyr Asn Cys Ile Asn Pro Ala Gly Ser Cys Thr Thr
   25           30           35           40

gcc atg aat tgt tca cat aat cag gat gcc tgt atc ttc gtt gaa gcc 257
Ala Met Asn Cys Ser His Asn Gln Asp Ala Cys Ile Phe Val Glu Ala
           45           50           55

gtg cca ccc aaa act tac tac cag tgt tgg agg ttc gat gaa tgc aat 305
Val Pro Pro Lys Thr Tyr Tyr Gln Cys Trp Arg Phe Asp Glu Cys Asn
           60           65           70

ttc gat ttc att tgc aga aac cta gcg gag aag aag ctg aag tac aac 353
Phe Asp Phe Ile Ser Arg Asn Leu Ala Glu Lys Lys Leu Lys Tyr Asn
           75           80           85

tgc tgc cgg aag gac ctg tgt aac aag agt gat gcc acg att tca tca 401
Cys Cys Arg Lys Asp Leu Cys Asn Lys Ser Asp Ala Thr Ile Ser Ser
           90           95          100

ggg aaa acc gct ctg ctg gtg atc ctg ctg ctg gta gca acc tgg cac 449
Gly Lys Thr Ala Leu Leu Val Ile Leu Leu Leu Val Ala Thr Trp His
   105           110           115           120

ttt tgt ctc taactgtaca ccaggagagt ttctcctcaa cttcctctgt 498
Phe Cys Leu

ctctctgttc ctatttccca tgctgcggtg ttccaaaggc tgtgtatgct ccagcttctt 558

cctgttggga aggactaaac ctagcttgag cactttggat tagagagaga aactttgagc 618

gactttgaag accaggcctg ttggcagaga agacctgtca gaggggaaac gttttaagag 678

tgaagcacag gtgatttgag cgaggcctat gcgtcttcct ctgctcttgg caggaccagc 738

tttgcggtaa ccattcgata gattccacaa tcctt 773
```

<210> 3

<211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 3  
 tgytayaayt gyathaa 17  
  
 <210> 4  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 4  
 agrtcytyyt krcarca 17  
  
 <210> 5  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 5  
 ccagtgcgca gagtgacgag gactcgagct caagct 36  
  
 <210> 6  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 6  
 ccagtgcgca gagtgacg 18  
  
 <210> 7  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 7  
 gaggactcga gctcaagc 18

<210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 8  
 tgcactacgg ccatgaattg 20  
  
 <210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 9  
 tcgttgaagc cgtgccaccc 20  
  
 <210> 10  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 10  
 aggtccttct tgcagcagtg 20  
  
 <210> 11  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 11  
 cttctccgct aggtttctcg 20  
  
 <210> 12  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer

<400> 12  
gcattcatcg aacctccaac 20

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
ggttctagag tagcgctgca gccggac 27

<210> 14  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
ggtggatcct tctctgccaa caggcct 27

<210> 15  
<211> 1637  
<212> DNA  
<213> Porcus sp.

<220>  
<221> modified\_base  
<222> (17)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1323)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1330)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1357)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1378)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1403)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1424)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1437)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1445)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1513)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1520)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1527)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1535)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1544)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1563)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1588)

<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1609)..(1611)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1625)  
<223> a, t, c, g, other or unknown

<400> 15  
ccaccgcggt ggcggcncgc tctagaacta gtggatcccc cgggctgcag gaattcggca 60  
cgagatttcg tcttaatcgc ggaggtcgca gagtcgggga gccgctcggg gtccccgttc 120  
ccgcgcgcca tgagtcacct gccgcggagc gccccgcggg tgaggcgctt aatgggcgga 180  
cagacgcgcg cgcgcgtgct gctgctgctg ctgctgctgt gtatcccggc tgcgcagggt 240  
gactgcagcc ttccaccoga tgtacctaat gcccaaccag atttgcgagg tcttgcaagt 300  
tttcctgaac aaaccacaat aacatacaaa tgtaacaaag gctttgtcaa agttcctggc 360  
atggcagact cagtgtctctg tcttaatgat aaatggtcag aagttgcaga attttgtaat 420  
cgtagctgtg atgttccaac caggctacat tttgcatctc ttaaaaagtc ttacagcaaa 480  
cagaattatt tcccagaggg ttccaccgtg gaatatgagt gccgtaaggg ctataaaagg 540  
gatcttactc tatcagaaaa actaacttgc cttcagaatt ttacgtgggc caaacctgat 600  
gaattttgca aaaaaaaaca atgtccgact cctggagaac taaaaaatgg tcatgtcaat 660  
ataacaactg acttggtatt tggcgcatcc atctttttct catgtaacgc aggttacaga 720  
ctagttgggt caacttctag ttactgtttt gccatagcaa atgatgttga gtggagtgat 780  
ccattgccag attgccaaga aatttctcca actgtcaaag ccataccagc tgttgagaaa 840  
cccatcacag taaattttcc agcaacaaag tatccagcta tcccaggggc cacaacgagt 900  
tttcattcaa gtacatctaa aaatcgagga aacccttctt caggcatgag aatcatgtcg 960  
tctggtacca tgctacttat tgcaggaggt gttgctgtta ttataataat tgttgcccta 1020  
attctagcca aaggtttctg gcactatgga aaatcaggct cttaccacac tcatgagAAC 1080  
aacaagccg ttaatgttgc attttataat ttacctgcga ctggcgatgc cgcagatgta 1140  
agacctggtA attaacaaaa ggacgtgcat gtgtaacact gacagttttg cttatgggtgc 1200  
tagtaaccat tggctagctg acttagccaa agaagagtta agaagaaagt gcacacaagt 1260  
acacagaata ttttcagttt cttaaaaact tcagggtggga gtggacatag tttgtggtag 1320  
tgntcttcgn tttgcatggt ttcattggct ctaaggnaca taggaatgca cagaaccnaa 1380  
gagaaacaaa tctatcctga aantacatcc tcaacacttc taanactctt ggaaatngaa 1440  
caagntcata agattgggag caattacttt cccaaaaggg tgagaaaaat ggagaaattt 1500  
ggtcatgggt agnaattttt gaaaaangaa acccnaaagg gganttttcc cccccaagg 1560  
ggnaagggtA tttttattta attaaggnaa aaaaaaaaaa aaaaaccnnn ngggggggcc 1620  
cgggncccat tttccct 1637

<210> 16  
<211> 978  
<212> DNA  
<213> Porcus sp.

<400> 16  
cacgagccgc cgcgcgtgct gctgctgctg ctgctgctgt gtatcccggc tgcgcagggt 60  
gactgcagcc ttccaccoga tgtacctaat gcccaaccag atttgcgagg tcttgcaagt 120  
tttcctgaac aaaccacaat aacatacaaa tgtaacaaag gctttgtcaa agttcctggc 180  
atggcagact cagtgtctctg tcttaatgat aaatggtcag aagttgcaga attttgtaat 240  
cgtagctgtg atgttccaac caggctacat tttgcatctc ttaaaaagtc ttacagcaaa 300  
cagaattatt tcccagaggg ttccaccgtg gaatatgagt gccgtaaggg ctataaaagg 360  
gatcttactc tatcagaaaa actaacttgc cttcagaatt ttacgtgggc caaacctgat 420  
gaattttgca aaaaaaaaca atgtccgact cctggagaac taaaaaatgg tcatgtcaat 480  
ataacaactg acttggtatt tggcgcatcc atctttttct catgtaacgc aggttacaga 540  
ctagttgggt caacttctag ttactgtttt gccatagcaa atgatgttga gtggagtgat 600

```

ccattgccag aatgccaaga aattttctcca actgtcaaag ccataaccagc tgttgagaaa 660
cccatcacag taaattttcc aggtaccaa ggcctatcat ctctcagaa accctccaca 720
gcaaatactc tagctacaga gttactacca actcctcagg aaccaccac agtaaagtgt 780
ccagatagta aagccatata atctctcag aaacctcca cagtaaatac tccagctaca 840
gacttactac caactcctca ggaaccacc acagtaaatag ttccagatag taaagccata 900
tcattcttctc agaaaccctc cacagtaaata actccagctc agacttacta ccaactcctc 960
aggaaccacc cacagtaa 978

```

```

<210> 17
<211> 327
<212> PRT
<213> Porcus sp.

```

```

<220>
<221> MOD_RES
<222> (322)
<223> Any amino acid

```

```

<400> 17
Met Gly Gly Gln Thr Pro Pro Pro Leu Leu Leu Leu Leu Leu Leu Leu
  1              5              10              15

Cys Ile Pro Ala Ala Gln Gly Asp Cys Ser Leu Pro Pro Asp Val Pro
      20              25              30

Asn Ala Gln Pro Asp Leu Arg Gly Leu Ala Ser Phe Pro Glu Gln Thr
      35              40              45

Thr Ile Thr Tyr Lys Cys Asn Lys Gly Phe Val Lys Val Pro Gly Met
      50              55              60

Ala Asp Ser Val Leu Cys Leu Asn Asp Lys Trp Ser Glu Val Ala Glu
      65              70              75              80

Phe Cys Asn Arg Ser Cys Asp Val Pro Thr Arg Leu His Phe Ala Ser
      85              90              95

Leu Lys Lys Ser Tyr Ser Lys Gln Asn Tyr Phe Pro Glu Gly Phe Thr
      100             105             110

Val Glu Tyr Glu Cys Arg Lys Gly Tyr Lys Arg Asp Leu Thr Leu Ser
      115             120             125

Glu Lys Leu Thr Cys Leu Gln Asn Phe Thr Trp Ser Lys Pro Asp Glu
      130             135             140

Phe Cys Lys Lys Lys Gln Cys Pro Thr Pro Gly Glu Leu Lys Asn Gly
      145             150             155             160

His Val Asn Ile Thr Thr Asp Leu Leu Phe Gly Ala Ser Ile Phe Phe
      165             170             175

Ser Cys Asn Ala Gly Tyr Arg Leu Val Gly Ala Thr Ser Ser Tyr Cys
      180             185             190

Phe Ala Ile Ala Asn Asp Val Glu Trp Ser Asp Pro Leu Pro Asp Cys

```



| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Glu | Ile | Ser | Pro | Thr | Val | Lys | Ala | Ile | Pro | Ala | Val | Glu | Lys | Pro |  |
| 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |
| Ile | Thr | Val | Asn | Phe | Pro | Ala | Thr | Lys | Tyr | Pro | Ala | Ile | Pro | Arg | Ala |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Thr | Thr | Ser | Phe | His | Ser | Ser | Thr | Ser | Lys | Asn | Arg | Gly | Asn | Pro | Ser |  |
| 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     |     |  |
| Ser | Gly | Met | Arg | Ile | Met | Ser | Ser | Gly | Thr | Met | Leu | Leu | Ile | Ala | Gly |  |
| 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |     |  |
| Gly | Val | Ala | Val | Ile | Ile | Ile | Ile | Ile | Val | Ala | Leu | Ile | Leu | Ala | Lys |  |
| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |     |  |
| Phe | Trp | His | Tyr | Gly | Lys | Ser | Gly | Ser | Tyr | His | Thr | His | Glu | Asn | Asn |  |
| 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |  |
| Lys | Ala | Val | Asn | Val | Ala | Phe | Tyr | Asn | Leu | Pro | Ala | Thr | Gly | Asp | Ala |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Ala | Xaa | Val | Arg | Pro | Gly | Asn |     |     |     |     |     |     |     |     |     |  |
| 325 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

<210> 18  
 <211> 325  
 <212> PRT  
 <213> Porcus sp.

|          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 18 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| His      | Glu | Pro | Pro | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Cys | Ile | Pro |  |
| 1        |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ala      | Ala | Gln | Gly | Asp | Cys | Ser | Leu | Pro | Pro | Asp | Val | Pro | Asn | Ala | Gln |     |  |
| 20       |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |     |  |
| Pro      | Asp | Leu | Arg | Gly | Leu | Ala | Ser | Phe | Pro | Glu | Gln | Thr | Thr | Ile | Thr |     |  |
| 35       |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |     |  |
| Tyr      | Lys | Cys | Asn | Lys | Gly | Phe | Val | Lys | Val | Pro | Gly | Met | Ala | Asp | Ser |     |  |
| 50       |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |     |  |
| Val      | Leu | Cys | Leu | Asn | Asp | Lys | Trp | Ser | Glu | Val | Ala | Glu | Phe | Cys | Asn |     |  |
| 65       |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Arg      | Ser | Cys | Asp | Val | Pro | Thr | Arg | Leu | His | Phe | Ala | Ser | Leu | Lys | Lys |     |  |
| 85       |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |     |     |  |
| Ser      | Tyr | Ser | Lys | Gln | Asn | Tyr | Phe | Pro | Glu | Gly | Phe | Thr | Val | Glu | Tyr |     |  |
| 100      |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |     |  |
| Glu      | Cys | Arg | Lys | Gly | Tyr | Lys | Arg | Asp | Leu | Thr | Leu | Ser | Glu | Lys | Leu |     |  |
| 115      |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |     |  |

Thr Cys Leu Gln Asn Phe Thr Trp Ser Lys Pro Asp Glu Phe Cys Lys  
 130 135 140  
 Lys Lys Gln Cys Pro Thr Pro Gly Glu Leu Lys Asn Gly His Val Asn  
 145 150 155 160  
 Ile Thr Thr Asp Leu Leu Phe Gly Ala Ser Ile Phe Phe Ser Cys Asn  
 165 170 175  
 Ala Gly Tyr Arg Leu Val Gly Ala Thr Ser Ser Tyr Cys Phe Ala Ile  
 180 185 190  
 Ala Asn Asp Val Glu Trp Ser Asp Pro Leu Pro Glu Cys Gln Glu Ile  
 195 200 205  
 Ser Pro Thr Val Lys Ala Ile Pro Ala Val Glu Lys Pro Ile Thr Val  
 210 215 220  
 Asn Phe Pro Gly Thr Lys Ala Leu Ser Ser Pro Gln Lys Pro Ser Thr  
 225 230 235 240  
 Ala Asn Thr Leu Ala Thr Glu Leu Leu Pro Thr Pro Gln Glu Pro Thr  
 245 250 255  
 Thr Val Asn Val Pro Asp Ser Lys Ala Ile Ser Ser Pro Gln Lys Pro  
 260 265 270  
 Ser Thr Val Asn Thr Pro Ala Thr Asp Leu Leu Pro Thr Pro Gln Glu  
 275 280 285  
 Pro Thr Thr Val Asn Val Pro Asp Ser Lys Ala Ile Ser Ser Ser Gln  
 290 295 300  
 Lys Pro Ser Thr Val Asn Thr Pro Ala Gln Thr Tyr Tyr Gln Leu Leu  
 305 310 315 320  
 Arg Asn Pro Pro Gln  
 325

<210> 19  
 <211> 376  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
 Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu Leu Pro Arg Leu  
 1 5 10 15  
 Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly Asp Cys Gly  
 20 25 30  
 Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly Arg Thr  
 35 40 45  
 Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser Phe  
 50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Lys | Ile | Pro | Gly | Glu | Lys | Asp | Ser | Val | Thr | Cys | Leu | Lys | Gly | Met |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gln | Trp | Ser | Asp | Ile | Glu | Glu | Phe | Cys | Asn | Arg | Ser | Cys | Glu | Val | Pro |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Thr | Arg | Leu | Asn | Ser | Ala | Ser | Leu | Lys | Gln | Pro | Tyr | Ile | Thr | Gln | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Phe | Pro | Val | Gly | Thr | Val | Val | Glu | Tyr | Glu | Cys | Arg | Pro | Gly | Tyr |  |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Arg | Arg | Glu | Pro | Ser | Leu | Ser | Pro | Lys | Leu | Thr | Cys | Leu | Gln | Asn | Leu |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Trp | Ser | Thr | Ala | Val | Glu | Phe | Cys | Lys | Lys | Lys | Ser | Cys | Pro | Asn |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Pro | Gly | Glu | Ile | Arg | Asn | Gly | Gln | Ile | Asp | Val | Pro | Gly | Gly | Ile | Leu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Phe | Gly | Ala | Thr | Ile | Ser | Phe | Ser | Cys | Asn | Thr | Gly | Tyr | Lys | Leu | Phe |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly | Ser | Thr | Ser | Ser | Phe | Cys | Leu | Ile | Ser | Gly | Ser | Ser | Val | Gln | Trp |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ser | Asp | Pro | Leu | Pro | Glu | Cys | Arg | Glu | Ile | Tyr | Cys | Pro | Ala | Pro | Pro |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Gln | Ile | Asp | Asn | Gly | Ile | Ile | Gln | Gly | Glu | Arg | Asp | His | Tyr | Gly | Tyr |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Arg | Gln | Ser | Val | Thr | Tyr | Ala | Cys | Asn | Lys | Gly | Phe | Thr | Met | Ile | Gly |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Glu | His | Ser | Ile | Tyr | Cys | Thr | Val | Asn | Asn | Asp | Glu | Gly | Glu | Trp | Ser |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Gly | Pro | Pro | Pro | Glu | Cys | Arg | Gly | Lys | Ser | Leu | Thr | Ser | Lys | Val | Pro |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Pro | Thr | Val | Gln | Lys | Pro | Thr | Thr | Val | Asn | Val | Pro | Thr | Thr | Glu | Val |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ser | Pro | Thr | Ser | Gln | Lys | Thr | Thr | Thr | Lys | Thr | Thr | Thr | Pro | Asn | Ala |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Gln | Ala | Thr | Arg | Ser | Thr | Pro | Val | Ser | Arg | Thr | Thr | Lys | His | Phe | His |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Glu | Thr | Thr | Pro | Asn | Lys | Gly | Ser | Gly | Thr | Thr | Ser | Gly | Thr | Thr | Arg |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Leu | Leu | Ser | Gly | His | Thr | Cys | Phe | Thr | Leu | Thr | Gly | Leu | Leu | Gly | Thr |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |

Leu Val Thr Met Gly Leu Leu Thr  
370 375

<210> 20  
<211> 128  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu  
1 5 10 15  
Ala Val Phe Cys His Ser Gly His Ser Leu Gln Cys Tyr Asn Cys Pro  
20 25 30  
Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe  
35 40 45  
Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys  
50 55 60  
Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg  
65 70 75 80  
Glu Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe  
85 90 95  
Asn Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val  
100 105 110  
Leu Leu Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro  
115 120 125

<210> 21  
<211> 126  
<212> PRT  
<213> Rattus sp.

<400> 21  
Met Arg Ala Arg Arg Gly Phe Ile Leu Leu Leu Leu Leu Ala Val Leu  
1 5 10 15  
Cys Ser Thr Gly Val Ser Leu Arg Cys Tyr Asn Cys Leu Asp Pro Val  
20 25 30  
Ser Ser Cys Lys Thr Asn Ser Thr Cys Ser Pro Asn Leu Asp Ala Cys  
35 40 45  
Leu Val Ala Val Ser Gly Lys Gln Val Tyr Gln Gln Cys Trp Arg Phe  
50 55 60  
Ser Asp Cys Asn Ala Lys Phe Ile Leu Ser Arg Leu Glu Ile Ala Asn  
65 70 75 80

Val Gln Tyr Arg Cys Cys Gln Ala Asp Leu Cys Asn Lys Ser Phe Glu  
85 90 95

Asp Lys Pro Asn Asn Gly Ala Ile Ser Leu Leu Gly Lys Thr Ala Leu  
100 105 110

Leu Val Thr Ser Val Leu Ala Ala Ile Leu Lys Pro Cys Phe  
115 120 125

<210> 22  
<211> 123  
<212> PRT  
<213> Murine sp.

<400> 22  
Met Arg Ala Gln Arg Gly Leu Ile Leu Leu Leu Leu Leu Ala Val  
1 5 10 15

Phe Cys Ser Thr Ala Val Ser Leu Thr Cys Tyr His Cys Phe Gln Pro  
20 25 30

Val Val Ser Ser Cys Asn Met Asn Ser Thr Cys Ser Pro Asp Gln Asp  
35 40 45

Ser Cys Leu Tyr Ala Val Ala Gly Met Gln Val Tyr Gln Arg Cys Trp  
50 55 60

Lys Gln Ser Asp Cys His Gly Glu Ile Ile Met Asp Gln Leu Glu Glu  
65 70 75 80

Thr Lys Leu Lys Phe Arg Cys Cys Gln Phe Asn Leu Cys Asn Lys Ser  
85 90 95

Asp Gly Ser Leu Gly Lys Thr Pro Leu Leu Gly Thr Ser Val Leu Val  
100 105 110

Ala Ile Leu Asn Leu Cys Phe Leu Ser His Leu  
115 120

<210> 23  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 23  
Cys Cys Lys Lys Asp Leu  
1 5

<210> 24  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative peptide

<220>

<221> MOD\_RES

<222> (7)

<223> Any amino acid

<220>

<221> MOD\_RES

<222> (10)

<223> Any amino acid

<400> 24

Asp Cys Gly Leu Pro Pro Xaa Val Pro Xaa Ala Gln Pro Ala  
1 5 10